

~~W/A~~
SEQUENCE LISTING

<110> Grainger, David J.
Tatalick, Lauen Marie

<120> Compounds and methods to inhibit or
augment an inflammatory response.

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<141> 1997-09-11

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Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
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Pro Lys Thr

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35 40 45
Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
50 55 60
Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
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35 40 45
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
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35 40 45
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
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Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe

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Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
35 40 45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
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35 40 45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
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Glu Asn Ser

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35 40 45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
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35 40 45
Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe
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Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp
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Pro

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35 40 45
Glu Ser Tyr Lys Arg Ile Thr Ser Ser Arg Cys Pro Lys Glu Ala Val
50 55 60
Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala Asp Pro Lys Lys
65 70 75 80
Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg Asn Gln Met Arg
85 90 95

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Ser	Arg	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Arg	Thr	Lys	Leu	Gly	Lys	
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His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
90 95

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Met Asn Pro Ser Ala Ala Val Ile

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 ctc gca agg acg gtc cgc tgc aac tgc atc cat atc gat gac ggg cca Leu Ala Arg Thr Val Arg Cys Asn Cys Ile His Ile Asp Asp Gly Pro 25	2724		
 gtg aga atg agg gcc ata ggg aag ctt gaa atc atc cct gcg agc cta Val Arg Met Arg Ala Ile Gly Lys Leu Glu Ile Ile Pro Ala Ser Leu 40	2772		
 tcc tgc cca cgt gtt gag atc at gtgagtacaa gcccacctgc cgataaacgt Ser Cys Pro Arg Val Glu Ile Ile 60	2825		
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 aaa aag aat gat gag cag aga tgt ctg aat ccg gaa tct aag acc atc Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys Thr Ile 70	3047		
 aag aat tta atg aaa gcg ttt agc caa aaa ag gtaggtttga tgttgcttt Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg 85	3099		
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Met Ala Arg Ala

1

acg	ctc	tcc	gcc	ccc	agc	aat	ccc	cgg	ctg	gtg	gct	ctg	102		
Thr	Leu	Ser	Ala	Ala	Pro	Ser	Asn	Pro	Arg	Leu	Leu	Arg	Val	Ala	Leu
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Leu	Leu	Leu	Leu	Leu	Val	Ala	Ala	Ser	Arg	Arg	Ala	Ala	Gly	Ala	Pro	
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Leu	Ala	Thr	Glu	Leu	Arg	Cys	Gln	Cys	Leu	Gln	Thr	Leu	Gln	Gly	Ile	
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His	Leu	Lys	Asn	Ile	Gln	Ser	Val	Lys	Val	Lys	Ser	Pro	Gly	Pro	His	
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tgc	gcc	caa	acc	gaa	gtc	ata	gcc	aca	ctc	aag	aat	ggg	cag	aaa	gct	294
Cys	Ala	Gln	Thr	Glu	Val	Ile	Ala	Thr	Leu	Lys	Asn	Gly	Gln	Lys	Ala	
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tgt	ctc	aac	ccc	gca	tcg	ccc	atg	gtt	aag	aaa	atc	atc	gaa	aag	atg	342
Cys	Leu	Asn	Pro	Ala	Ser	Pro	Met	Val	Lys	Lys	Ile	Ile	Glu	Lys	Met	
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Leu Lys Asn Gly Lys Ser Asn
105

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Met Ser Leu
1

ctg tcc agc cgc gcg gcc cgt gtc ccc ggt cct tcg agc tcc ttg tgc 163
Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser Ser Leu Cys
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gcg ctg ttg gtg ctg ctg ctg acg cag cca ggg ccc atc gcc 211
Ala Leu Leu Val Leu Leu Leu Thr Gln Pro Gly Pro Ile Ala
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Ser Ala Gly Pro Ala Ala Val Leu Arg Glu Leu Arg Cys Val Cys
40 45 50

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Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser Asn Leu Gln
55 60 65

gtg ttc gcc ata ggc cca cag tgc tcc aag gtg gaa gtg gta gcc tcc 355
Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser
70 75 80

ctg aag aac ggg aag gaa att tgt ctt gat cca gaa gcc cct ttt cta 403

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Lys	Lys	Val	Ile	Gln	Lys	Ile	Leu	Asp	Gly	Gly	Asn	Lys	Glu	Asn			
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Leu	Cys	Leu	Leu	Leu	Met	Thr	Ala	Ala	Phe	Asn	Pro	Gln	Gly	Leu	Ala		
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cag	cca	gat	gca	ctc	aac	gtc	cca	tct	act	tgc	tgc	ttc	aca	ttt	agc		150
Gln	Pro	Asp	Ala	Leu	Asn	Val	Pro	Ser	Thr	Cys	Cys	Phe	Thr	Phe	Ser		
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Ser	Lys	Lys	Ile	Ser	Leu	Gln	Arg	Leu	Lys	Ser	Tyr	Val	Ile	Thr	Thr		
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agc	agg	tgt	ccc	cag	aag	gct	gtc	atc	ttc	aga	acc	aaa	ctg	ggc	aag		246
Ser	Arg	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Arg	Thr	Lys	Leu	Gly	Lys		
60					65								70				
gag	atc	tgt	gct	gac	cca	aag	gag	aag	tgg	gtc	cag	aat	tat	atg	aaa		294
Glu	Ile	Cys	Ala	Asp	Pro	Lys	Glu	Lys	Trp	Val	Gln	Asn	Tyr	Met	Lys		

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His Leu Gly Arg Lys Ala His Thr Leu Lys Thr			
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Asn Gln Val Leu Ser Ala Pro	
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Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys	
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Phe Leu Thr Lys Arg Gly Arg	
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Asp Leu Glu Leu Ser Ala	
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 Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile Ala
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 Glu Cys Cys Phe Thr Tyr Thr Tyr Lys Ile Pro Arg Gln Arg Ile
 35 40 45

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 Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile Val
 50 55 60 65

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 Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp Lys
 70 75 80

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 Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
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caa gag att ccc ctg agg gca atc ctg tgt tac aga aat acc agc tcc	2237		
Gln Glu Ile Pro Leu Arg Ala Ile Leu Cys Tyr Arg Asn Thr Ser Ser			
40	45	50	55
atc tgc tcc aat gag ggc tta at gtaagtgatc acctgctcaa tctctcccta	2290		
Ile Cys Ser Asn Glu Gly Leu Ile			
60			
gagaacagaa cccgccagc ctggattac aagatggac actagatgac agtattttac	2350		
tggaaataagg ttctaaacc cagagctgcc agcacctggg tgcaagccac acttggcg	2410		
tagagggagc gctgagcttc ctgcgggtg tgaggaagga tgcatctgtg ctccctgcagt	2470		
ggcttggat ttctgaaact ccaagggtcc aagtattgtt tcccgccatt atgagctcag	2530		
aggtttaaca aaagcatgag gggattttgt gcactggaaa gagcaaggaa accaggatga	2590		
gttcctgccc ctggattttgg aaccatagt cttgggtgac cgtggacagg taactccctt	2650		
gtactgaatt gtctgttat cttctgtat tccttatctg tgaagggtca taaacatagc	2710		
tgcatcacag ggtcttaca aacttaattt gagtagctt cacataccag tcagtatttt	2770		
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tagagtttgt ctatagattt gacaatagtc cagtttaga agtagacaga tcagaagaga	2950		
aaaatacaca cccacacaca cacacaaggc gcgcgcacac acacacacaa aacacatga	3010		
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gcggggctt gtcgttgccc acccagtggt ggctgggtg gctcagccctt ctcttattt	3370		
ctctgttccac ag a ttc aag ctg aag aga ggc aaa gag gcc tgc gcc ttg	3419		
Phe Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu			
65	70	75	
gac aca gtt gga tgg gtt cag agg cac aga aaa atg ctg agg cac tgc	3467		
Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met Leu Arg His Cys			
80	85	90	
ccg tca aaa aga aaa tgagcagatt tctttccatt tggtggctctg gaaaccacat	3522		
Pro Ser Lys Arg Lys			
95			
ggttcacct gtccccggaa ctaccagccc tacaccattt cttctggccct gctttgcta	3582		
ggtcacagag gatctgcttg gtcttgataa gctatgtgt tgcactttaa acatttaat	3642		
tataacaatca tcaaccccca accctctggg ctcttgatt tcagagtgaa aacttgatgg	3702		
cattgag	3709		

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<210> 37
<211> 673
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (67) ... (450)

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    Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala
    1           5           10
                    15          20          25          30
aga cca ctt cat gcc ttg cag gtg ctg ctg ctt ctg tca ttg ctg ctg 156
Arg Pro Leu His Ala Leu Gln Val Leu Leu Leu Leu Ser Leu Leu Leu
    15          20          25          30
                    35          40          45
act gct ctg gct tcc tcc acc aaa gga caa act aag aga aac ttg gcg 204
Thr Ala Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala
    35          40          45
                    50          55          60
aaa ggc aaa gag gaa agt cta gac agt gac ttg tat gct gaa ctc cgc 252
Lys Gly Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg
    50          55          60
                    65          70          75
tgc atg tgt ata aag aca acc tct gga att cat ccc aaa aac atc caa 300
Cys Met Cys Ile Lys Thr Ser Gly Ile His Pro Lys Asn Ile Gln
    65          70          75
                    80          85          90
agt ttg gaa gtg atc ggg aaa gga acc cat tgc aac caa gtc gaa gtg 348
Ser Leu Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val
    80          85          90
                    95          100          105          110
ata gcc aca ctg aag gat ggg agg aaa atc tgc ctg gac cca gat gct 396
Ile Ala Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala
    95          100          105
                    115          120          125
ccc aga atc aag aaa att gta cag aaa aaa ttg gca ggt gat gaa tct 444
Pro Arg Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser
    115          120
                    125
gct gat taatttgttc tgtttctgcc aaacttcttt aactcccagg aagggttagaa 500
Ala Asp
                    550          560          570          580          590          600          610          620          630          640          650          660          670          680          690          700          710          720          730          740          750          760          770          780          790          800          810          820          830          840
ttttgaaacc ttgattttct agagttctca tttattcagg atacccattc ttactgtatt 560
aaaatttggaa tatgtgtttc attctgtctc aaaaatcaca ttttattctg agaagggttg 620
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<210> 38

<211> 12
<212> PRT
<213> Homo sapiens

<400> 38
Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
1 5 10

<210> 39
<211> 2545
<212> DNA
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<220>
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<222> (40) ... (414)

<400> 39

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Met Lys Lys Ser Gly
1 5

gtt ctt ttc ctc ttg ggc atc atc ttg ctg gtt ctg att gga gtg caa 102
Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val Leu Ile Gly Val Gln
10 15 20

gga acc cca gta gtg aga aag ggt cgc tgt tcc tgc atc agc acc aac 150
Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn
25 30 35

caa ggg act atc cac cta caa tcc ttg aaa gac ctt aaa caa ttt gcc 198
Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp Leu Lys Gln Phe Ala
40 45 50

cca agc cct tcc tgc gag aaa att gaa atc att gct aca ctg aag aat 246
Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ala Thr Leu Lys Asn
55 60 65

gga gtt caa aca tgt cta aac cca gat tca gca gat gtg aag gaa ctg 294
Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala Asp Val Lys Glu Leu
70 75 80 85

att aaa aag tgg gag aaa cag gtc agc caa aag aaa aag caa aag aat 342
Ile Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn
90 95 100

ggg aaa aaa cat caa aaa aag aaa gtt ctg aaa gtt cga aaa tct caa 390
Gly Lys His Gln Lys Lys Val Leu Lys Val Arg Lys Ser Gln
105 110 115

cgt tct cgt caa aag aag act aca taagagacca cttcaccaat aagtattctg 444
Arg Ser Arg Gln Lys Lys Thr Thr
120 125

tgttaaaaat gttctattt aattataccg ctatcattcc aaaggaggat ggcataaat	504
acaaaggc tttagaaatgat attaatttga ctagaaaatt taaaacatta ctctgaaatt gtaactaaag	564
tttagaaatgat gattttaga atccaaacgt taagaattgt taaaggctat gattgtctt	624
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gaagtactaa gcgctagagg aagcagccaa gtcggtagt ggaagcatga ttgggtccca	2064
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<210> 41
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 <212> PRT
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<400> 41

Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys
1 5 10

<210> 42
<211> 12
<212> PRT
<213> Homo sapiens

Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
1 5 10

<210> 43
<211> 12
<212> PRT
<213> Homo sapiens

Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Homo sapiens

Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
1 5 10

<210> 45
<211> 125
<212> PRT
<213> Homo sapiens

<400> 45
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1 5 10 15
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20 25 30
Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
35 40 45
Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
50 55 60
Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
65 70 75 80
Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
85 90 95
Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
100 105 110
Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
115 120 125

<210> 46
<211> 128
<212> PRT
<213> Homo sapiens

<400> 46

Met	Ser	Leu	Arg	Leu	Asp	Thr	Thr	Pro	Ser	Cys	Asn	Ser	Ala	Arg	Pro
1			5					10					15		
Leu	His	Ala	Leu	Gln	Val	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Thr	Ala	
			20					25					30		
Leu	Ala	Ser	Ser	Thr	Lys	Gly	Gln	Thr	Lys	Arg	Asn	Leu	Ala	Lys	Gly
		35			40				45						
Lys	Glu	Glu	Ser	Leu	Asp	Ser	Asp	Leu	Tyr	Ala	Glu	Leu	Arg	Cys	Met
				50		55				60					
Cys	Ile	Lys	Thr	Thr	Ser	Gly	Ile	His	Pro	Lys	Asn	Ile	Gln	Ser	Leu
		65			70				75				80		
Glu	Val	Ile	Gly	Lys	Gly	Thr	His	Cys	Asn	Gln	Val	Glu	Val	Ile	Ala
			85					90				95			
Thr	Leu	Lys	Asp	Gly	Arg	Lys	Ile	Cys	Leu	Asp	Pro	Asp	Ala	Pro	Arg
		100					105				110				
Ile	Lys	Lys	Ile	Val	Gln	Lys	Lys	Leu	Ala	Gly	Asp	Glu	Ser	Ala	Asp
		115				120						125			

<210> 47
<211> 96
<212> PRT
<213> Homo sapiens

<400> 47

Met	Gln	Ile	Ile	Thr	Thr	Ala	Leu	Val	Cys	Leu	Leu	Leu	Ala	Gly	Met
1				5					10				15		
Trp	Pro	Glu	Asp	Val	Asp	Ser	Lys	Ser	Met	Gln	Val	Pro	Phe	Ser	Arg
				20				25				30			
Cys	Cys	Phe	Ser	Phe	Ala	Glu	Gln	Glu	Ile	Pro	Leu	Arg	Ala	Ile	Leu
			35			40				45					
Cys	Tyr	Arg	Asn	Thr	Ser	Ser	Ile	Cys	Ser	Asn	Glu	Gly	Leu	Ile	Phe
		50			55				60						
Lys	Leu	Lys	Arg	Gly	Lys	Glu	Ala	Cys	Ala	Leu	Asp	Thr	Val	Gly	Trp
		65			70				75			80			
Val	Gln	Arg	His	Arg	Lys	Met	Leu	Arg	His	Cys	Pro	Ser	Lys	Arg	Lys
				85				90				95			

<210> 48
<211> 93
<212> PRT
<213> Homo sapiens

<400> 48

Met	Lys	Ile	Ser	Val	Ala	Ala	Ile	Pro	Phe	Phe	Leu	Leu	Ile	Thr	Ile
1				5					10				15		
Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro
				20				25			30				
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg

35 40 45
Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile
50 55 60
Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp
65 70 75 80
Lys Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
85 90

<210> 49
<211> 93
<212> PRT
<213> Homo sapiens

<400> 49
Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
1 5 10 15
Leu Cys Asn Gln Val Leu Ser Ala Pro Leu Ala Ala Asp Thr Pro Thr
20 25 30
Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile
35 40 45
Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Ser Val Ile
50 55 60
Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu
65 70 75 80
Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
85 90

<210> 50
<211> 98
<212> PRT
<213> Homo sapiens

<400> 50
Met Lys Val Ser Ala Val Leu Leu Cys Leu Leu Leu Met Thr Ala Ala
1 5 10 15
Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser
20 25 30
Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
35 40 45
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile
50 55 60
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys
65 70 75 80
Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
85 90 95
Lys Thr

<210> 51
<211> 839
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (54) ... (344)

<400> 51

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5	10	15
agc ccc cag ggg ctc gct ggg cca gct tct gtc cca acc acc tgc tgc	Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys Cys	152
20	25	30
ttt aac ctg gcc aat agg aag ata ccc ctt cag cga cta gag agc tac	Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr	200
35	40	45
agg aga atc acc agt ggc aaa tgt ccc cag aaa gct gtg atc ttc aag	Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys	248
50	55	60
acc aaa ctg gcc aag gat atc tgt gcc gac ccc aag aag aag tgg gtg	Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val	296
70	75	80
cag gat tcc atg aag tat ctg gac caa aaa tct cca act cca aag cca	Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro	344
85	90	95
taaataatca ccattttga aaccaaacca gagcctgagt gttgccta at ttgtttccc		404
ttcttacaat gcattctgag gtaacctcat tattcgtcca aaggcatgg gttttattat		464
atatatatat atatatttt tttaaaaaaa aaacgtattt catttaattt attgaggctt		524
taaaaacttat cctccatgaa tattcgtttat ttttaactg taaagcttg tgcatattct		584
ttaccccttg ggagccccaa ttcatcccc ttgcacgtgt gggcaatgtt cccctctcc		644
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ttgttcttgt gaacccaaag ttgtactcat taaatggaaag taatgttgg ttaggaatac		764
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<210> 52

<211> 114

<212> PRT

<213> Homo sapiens

<400> 52

Met Ser Leu Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser			
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Ser Leu Cys Ala Leu Leu Val Leu Leu Leu Leu Thr Gln Pro Gly			
20	25	30	

Pro Ile Ala Ser Ala Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg
 35 40 45
 Cys Val Cys Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser
 50 55 60
 Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val
 65 70 75 80
 Val Ala Ser Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala
 85 90 95
 Pro Phe Leu Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys
 100 105 110
 Glu Asn

<210> 53
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 53
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 20 25 30
 Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35 40 45
 Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser
 50 55 60
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65 70 75 80
 Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile
 85 90 95
 Ile Glu Lys Met Leu Lys Asn Gly Lys Ser Asn
 100 105

<210> 54
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met Asn Pro Ser Ala Ala Val Ile Phe Cys Leu Ile Leu Leu Gly Leu
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 Ser Gly Thr Gln Gly Ile Pro Leu Ala Arg Thr Val Arg Cys Asn Cys
 20 25 30
 Ile His Ile Asp Asp Gly Pro Val Arg Met Arg Ala Ile Gly Lys Leu
 35 40 45
 Glu Ile Ile Pro Ala Ser Leu Ser Cys Pro Arg Val Glu Ile Ile Ala
 50 55 60
 Thr Met Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys
 65 70 75 80
 Thr Ile Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg Ser Lys Arg
 85 90 95
 Ala Pro

<210> 55
<211> 1041
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (18) ... (338)

<400> 55

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15 20 25	
gct ggc cgg cgc gca gca gga gcg tcc gtg gcc act gaa ctg cgc tgc Ala Gly Arg Arg Ala Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys	146
30 35 40	
cag tgc ttg cag acc ctg cag gga att cac ccc aag aac atc caa agt Gln Cys Leu Gln Thr Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser	194
45 50 55	
gtg aac gtg aag tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata Val Asn Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile	242
60 65 70 75	
gcc aca ctc aag aat ggg cgg aaa gct tgc ctc aat cct gca tcc ccc Ala Thr Leu Lys Asn Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro	290
80 85 90	
ata gtt aag aaa atc atc gaa aag atg ctg aac agt gac aaa tcc aac Ile Val Lys Lys Ile Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn	338
95 100 105	
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<400> 56

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20 25 30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
35 40 45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
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Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
85 90

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<400> 57

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20 25 30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
35 40 45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65 70 75 80
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85 90 95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
100 105

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<400> 58

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Met Thr Ser Lys Leu

60
116

1 5

gcc gtc gct ctc ttg gca gcc ttc ctg att tct gca gct ctg tgt gaa Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu	164
10 15 20	
ggt gca gtt ttg cca agg agt gct aaa gaa ctt aga tgt cag tgc ata Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile	212
25 30 35	
aag aca tac tcc aaa cct ttc cac ccc aaa ttt atc aaa gaa ctg aga Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg	260
40 45 50	
gtg att gag agt gga cca cac tgc gcc aac aca gaa att att gta aag Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys	308
55 60 65	
ctt tct gat gga aga gag ctc tgt ctg gac ccc aag gaa aac tgg gtg Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val	356
70 75 80 85	
cag agg gtt gtg gag aag ttt ttg aag agg gct gag aat tca Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser	398
90 95	
aaaaaaaaatt cattctctgt ggtatccaag aatcagtgaa gatggcagtg aaacttcaag caaatctact tcaacacttc atgtatttgt tggtctgtt gtagggttgc cagatcaat	458
acaagattcc tggtaaatt tgaatttcag taaacaatga atagttttc attgtaccat	518
gaaatatcca gaacatactt atatgtaaag tattatttat ttgaatctac aaaaaacaac	578
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cccagttaaa tttcatttc agatatacaa caaataatt ttttagtataa gtacatttt	1238
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1 5 10 15

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1 5 10 15

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1 5 10 15

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1 5 10 15

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1 5 10

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<400> 66
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1 5 10

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Glu Ile Cys Ala Asp Pro Lys Glu Arg Trp Val Arg
1 5 10

<210> 68
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1 5 10 15

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1 5 10 15

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1 5 10 15

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1 5 10 15

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1 5 10

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1 5 10

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Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln
1 5 10

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1 5 10

<210> 76
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Leu Cys Leu Leu Ile Ala Ala Thr Phe Ile Pro Gln Gly Leu Ala			
10 15 20			
cag cca gat gca atc aat gcc cca gtc acc tgc tgc tat aac ttc acc			148
Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe Thr			
25 30 35			
aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc acc			196
Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile Thr			
40 45 50 55			
agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg gcc			244
Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala			
60 65 70			
aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc atg			292
Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met			
75 80 85			
gac cac ctg gac aagcaa acc caact ceg aag act tga acactcactc			341
Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr *			
90 95			
cacaaccCAA gaatctgcAG ctaacttatt ttcccctAG tttccccAGA catccTgtTT			401
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acAGAGACTT gGGGAAATTg ctTTTcCTcT tGAACCACAG ttCTAACCCcT gggATgtTTT			581
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ccgcccGCCc gcccGcGCC AtG AAC GCC AAG GTC GTG GTC GTG CTG GTC CTC			112
Met Asn Ala Lys Val Val Val Val Leu Val Leu			
1 5 10			
gtG ctG acc GcG cTC tGc cTC AGC GAC GGG AAG CCC GTC AGC CTG AGC			160
Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser			
15 20 25			
tac aga tgc cca tgc cga ttc ttc gaa agc agc cat gtt gcc aga gcc aac			208

Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn
 30 35 40
 gtc aag cat cts aaa att ctc aac act cca aac tgt gcc ctt cag att 256
 Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile
 45 50 55
 gta gcc cggtg aag aac aac aac aga caa gtg tgc att gac ccg aag 304
 Val Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
 60 65 70 75
 cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag 346
 Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
 80 85
 taaggcacaac agccaaaaag gacttccgc tagaccact cgaggaaaac taaaaccttg 406
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Met Lys Val Ser Ala Ala Arg Leu Ala
1 5

gtc atc ctc att gct act gcc ctc tgc gct cct gca tct gcc tcc cca	101
Val Ile Leu Ile Ala Thr Ala Leu Cys Ala Pro Ala Ser Ala Ser Pro	
15 20 25	
tat tcc tcg gac acc aca ccc tgc tgc ttt gcc tac att gcc cgc cca	149
Tyr Ser Ser Asp Thr Thr Pro Cys Cys Phe Ala Tyr Ile Ala Arg Pro	
30 35 40	
ctg ccc cgt gcc cac atc aag gag tat ttc tac acc agt ggc aag tgc	197
Leu Pro Arg Ala His Ile Lys Glu Tyr Phe Tyr Thr Ser Gly Lys Cys	
45 50 55	
tcc aac cca gca gtc gtc ttt gtc acc cga aag aac cgc caa gtg tgt	245
Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln Val Cys	
60 65 70	
gcc aac cca gag aag aaa tgg gtt cgg gag tac atc aac tct ttg gag	293
Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser Leu Glu	
75 80 85	
atg agc taggatggag agtccttgaa cctgaactta cacaatttg cctgtttctg	349
Met Ser	
90	
cttgctttg tccttagcttg ggaggcttcc cctcaactatc ctacccacc cgctccttga	409
aggcccaga ttctgaccac gacgagcagc agttacaaaa accttccccca ggctgacgt	469
ggtggctcag ccttctaattc ccagcacttt gggaggccaa ggtgggtgga tcacttgagg	529
tcaggagttc gagacagcct gccaacatg atgaaacccc atgtgtacta aaaatacaa	589
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ccagcctggg tgacaaagtg agactccgtc acaacaacaa caacaaaaag cttcccaac	949
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Met Lys Leu	
1	
tgc gtg act gtc stg tct ctc ctc atg cta gta gct gcc ttc tgc tct	165
Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala Phe Cys Ser	
5 10 15	
cca gcg ctc tca gca cca atg ggc tca gac cct ccc acc gcc tgc tgc	213
Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys	
20 25 30 35	
ttt tct tac acc gcg agg aag ctt cct cgc aac ttt gtg gta gat tac	261
Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr	
40 45 50	
tat gag acc agc agc ctc tgc tcc cag cca gct gtg gta ttc caa acc	309
Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr	
55 60 65	
aaa aga agc aag caa gtc tgt gct gat ccc agt gaa tcc tgg gtc cag	357
Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln	
70 75 80	
gag tac gtg tat gac ctg gaa ctg aac tgagctgtc agagacagga	404
Glu Tyr Val Tyr Asp Leu Glu Leu Asn	
85 90	
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ctatggggat ggtccactgt cactgtttct ctgctgttgc aaatacatgg ataacacatt	644
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tt gct cag cca gat tca gtt tcc att cca atc acc tgc tgc ttt aac	
Ala Gln Pro Asp Ser Val Ile Pro Ile Thr Cys Cys Phe Asn	
1 5 10 15	
gtg atc aat agg aaa att cct atc cag agg ctg gag agc tac aca aga	215
Val Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg	
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gtaatcttac taagagctaa tagaaaggctt aggaccaaacc cagaaacacctc caattctcat 300
gtggaagccc atgcctcac cctccaaac atg aaa gcc tct gca gca ctt ctg 352
Met Lys Ala Ser Ala Ala Leu Leu
1 5

tgt ctg ctg ctc aca gca gct gct ttc agc ccc cag ggg ctt gct cag 400
Cys Leu Leu Leu Thr Ala Ala Phe Ser Pro Gln Gly Leu Ala Gln
10 15 20

cca gtt ggg att aat act tca act acc tgc tgc tac aga ttt atc aat 448
Pro Val Gly Ile Asn Thr Ser Thr Cys Cys Tyr Arg Phe Ile Asn
25 30 35 40

aag aaa atc cct aag cag agg ctg gag agc tac aga agg acc acc agt 496
Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser
45 50 55

agc cac tgt ccc cggtt gaa gct gta atc ttc aag acc aaa ctg gac aag 544
Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp Lys
60 65 70

gag atc tgt gct gac ccc aca cag aag tgg gtc cag gac ttt atg aag 592
Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met Lys
75 80 85

cac ctg gac aag aaa acc caa act cca aag ctt tgaacattca tgactgaact 645
His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
90 95

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Met Gln Val Ser Thr Ala Ala Leu Ala Val
1 5 10

60
113

ctc ctc tgc acc atg gct ctc tgc aac cag ttc tct gca tca ctt gct
Leu Leu Cys Thr Met Ala Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala
15 20 25

161

gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cgg cag att
Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile
30 35 40

209

cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc tcc
Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser
45 50 55

257

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Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln Val Cys Ala
60 65 70

305

gac ccc agt gag gag tgg gtc cag aaa tat gtc agc gac ctg gag ctg
Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu
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353

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Ser Ala

409

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529

589

649

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769

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<211> 98
<212> PRT
<213> Homo sapiens

<400> 83

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Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
35 40 45
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile
50 55 60
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys
65 70 75 80
Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
85 90 95
Lys Thr



Creation date: 02-26-2004

Indexing Officer: SKANNATHIP - SUTHAM KANNATHIP

Team: OIPEBackFileIndexing

Dossier: 08927939

Legal Date: 02-26-1999

No.	Doccode	Number of pages
1	CRFL	6

Total number of pages: 6

Remarks:

Order of re-scan issued on